

SEQUENCE LISTING

(1) GENERAL INFORMATION:

APPLICANT:

5 NAME: The Procter & Gamble Company
STREET: One Procter & Gamble Plaza
CITY: Cincinnati, OHIO
COUNTRY: USA
POSTAL CODE: 45202

10 TITLE OF INVENTION: Detergent compositions comprising a mannanase and a
soil release polymer.

NUMBER OF SEQUENCES: 6

15

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
20 SOFTWARE: PatentIn Release # 1.0 Version 1.25 (EPO)

SEQ ID NO:1

SEQUENCE CHARACTERISTICS:

25 LENGTH: 1407 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear

30 MOLECULE TYPE: genomic DNA
ORIGINAL SOURCE

FEATURE:

NAME/KEY: CDS
35 LOCATION: 1-1482

005040" 05958460

SEQUENCE DESCRIPTION: SEQ ID NO: 1

5 ATGAAAAAAAAAGTTATCACAGATTTATCATTTAATTATTTGCACACTTATAATA
AGTGTGGGAATAATGGGGATTACAACGTCCCCATCAGCAGCAAGTACAGGC
TTTTATGTTGATGGCAATACGTTATATGACGCAAATGGGCAGCCATTTGTCAT
GAGAGGTATTAACCATGGACATGCTTGGTATAAAGACACCGCTTCAACAGCT
ATTCCTGCCATTGCAGAGCAAGGCGCCAACACGATTCTGATTGTTTTATCAG
10 ATGGCGGTCAATGGGAAAAAGACGACATTGACACCATTCGTGAAGTCATTG
AGCTTGCGGAGCAAAATAAAATGGTGGCTGTCGTTGAAGTTCATGATGCCA
CGGGTCGCGATTGCGCGAGTGATTTAAATCGAGCCGTTGATTATTGGATAG
AAATGAAAGATGCGCTTATCGGTAAAGAAGATACGGTTATTATTAACATTGCA
AACGAGTGGTATGGGAGTTGGGATGGCTCAGCTTGGGCCGATGGCTATATT
15 GATGTCATTCCGAAGCTTCGCGATGCCGGCTTAACACACACCTTAATGGTTG
ATGCAGCAGGATGGGGGCAATATCCGCAATCTATTGATTACGGACAAG
GAGTATGCTGGTGGTATGCTAACACTGTTAGATCAAATATTGATAGAGTCA
TAGATCAAGACCTTGCTCTCGTAATAGGTGAATTCGGTCATAGACATACTGA
TGGTATGTTGATGAAGATAACAATCCTTAGTTATTCTGAAGAACTGGCACA
20 GGGTGGCTCGCTTGGTCTTGGAAAGGCAACAGTACCGAATGGGACTATTTA
GACCTTTCAGAAGACTGGGCTGGTCAACATTTAACTGATTGGGGGAATAGAA
TTGTCCACGGGGCCGATGGCTTACAGGAAACCTCCAAACCATCCACCGTAT
TGACTTTGAAGGAAGCACACAAGGGTGGCATGGAAGCAACGTGACCGGTG
25 GCCCTTGGTCCGTAACAGAATGGGGTGCTTCAGGTAACACTCTTTAAAAGC
CGATGTAAATTTAACCTCAAATTCTTCACATGAACTGTATAGTGAACAAAGTC
GTAATCTACACGGATACTCTCAGCTCAACGCAACCGTTCCGCATGCCAATTG
GGGAAATCCCGGTAATGGCATGAATGCAAGACTTTACGTGAAAACGGGCTC
TGATTATACATGGCATAGCGGTCTTTTACACGTATCAATAGCTCCAACCTCA
30 GGAACAACGTTATCTTTTGATTAAACAACATCGAAAATAGTCATCATGTTAG
GGAAATAGGCGTGCAATTTTCAGCGGCAGATAATAGCAGTGGTCAAACCTGC
TCTATACGTTGATAACGTTACTTTAAGATAG

7945450-040500

SEQ ID NO:2**5 SEQUENCE CHARACTERISTICS:**

LENGTH: 493 amino acids

TYPE: amino acid

TOPOLOGY: linear

10 MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 2

005040" 05958450

15 MKKKLSQIYHLIICTLIISVGIMGITTSPSAASTGFYVDGNTLYDANGQPFVMRGIN
HGHAWYKDTASTAIPAIAEQGANTIRIVLSGGQWEKDDIDTIREVIELAEQNKM
VAVVEVHDATGRDSRSDLNRAVDYWIEMKDALIGKEDTVIINIANEWYGSWDGS
AWADGYIDVIPKL RDAGLTHTLMVDAAGWGQYPQSIHDYGGQDVFNADPLKNTM
FSIHMYEYAGGDANTVRSNIDRVIDQDLALVIGEFGHRHTDGDVDEDTILSYSEE
TGTGWLAWSWKGNSTEWLDYLDLSEDWAGQHLTDWGNRIVHGADGLQETSKP
STVFTDDNGGHPEPPTATTLYDFEGSTQGWHGSNVTGGPWSVTEWGASGNY
20 SLKADVNLT SNSSHELYSEQSRNLHGYSQLNATVRHANWGNPGNGMNARLYV
KTGSDYTWHS GPFTRINSSNSGTTLSFDLNNIENSHHVREIGVQFSAADNSSGQ
TALYVDNVTLR

25 SEQ ID NO:3**SEQUENCE CHARACTERISTICS:**

LENGTH: 1407 base pairs

TYPE: nucleic acid

30 STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: genomic DNA

35 SEQUENCE DESCRIPTION: SEQ ID NO: 3

ATGAAAAAAAAAGTTATCACAGATTTATCATTTAATTATTTGCACACTTATAATA
AGTGTGGGAATAATGGGGATTACAACGTCCCCATCAGCAGCAAGTACAGGC
TTTTATGTTGATGGCAATACGTTATATGACGCAAATGGGCAGCCATTTGTCAT
GAGAGGTATTAACCATGGACATGCTTGGTATAAAGACACCGCTTCAACAGCT
5 ATTCCTGCCATTGCAGAGCAAGGCGCCAACACGATTCGTATTGTTTTATCAG
ATGGCGGTCAATGGGAAAAAGACGACATTGACACCATTTCGTGAAGTCATTG
AGCTTGCGGAGCAAAATAAAATGGTGGCTGTCGTTGAAGTTCATGATGCCA
CGGGTCGCGATTTCGCGCAGTGATTTAAATCGAGCCGTTGATTATTGGATAG
AAATGAAAGATGCGCTTATCGGTAAAGAAGATACGGTTATTATTAACATTGCA
10 AACGAGTGGTATGGGAGTTGGGATGGCTCAGCTTGGGCCGATGGCTATATT
GATGTCATTCCGAAGCTTCGCGATGCCGGCTTAACACACACCTTAATGGTTG
ATGCAGCAGGATGGGGGCAATATCCGCAATCTATTCATGATTACGGACAAG
ATGTGTTTAATGCAGATCCGTAAAAAATACGATGTTCTCCATCCATATGTAT
GAGTATGCTGGTGGTGAAGTAACTGTTAGATCAAATATTGATAGAGTCA
15 TAGATCAAGACCTTGCTCTCGTAATAGGTGAATTCGGTCATAGACATACTGA
TGGTGAAGTGAAGATAACAATCCTTAGTTATTCTGAAGAACTGGCACA
GGGTGGCTCGCTTGGTCTTGAAAGGCAACAGTACCGAATGGGACTATTTA
GACCTTTCAGAAGACTGGGCTGGTCAACATTTAACTGATTGGGGGAATAGAA
TTGTCCACGGGGCCGATGGCTTACAGGAAACCTCCAAACCATCCACCGTAT
20 TTACAGATGATAACGGTGGTCACCCTGAACCGCCAACTGCTACTACCTTGTA
TGACTTTGAAGGAAGCACACAAGGGTGGCATGGAAGCAACGTGACCGGTG
GCCCTTGGTCCGTAACAGAATGGGGTGCTTCAGGTAACCTACTCTTTAAAGC
CGATGTAAATTTAACCTCAAATTCTTCACATGAACTGTATAGTGAACAAAGTC
GTAATCTACACGGATACTCTCAGCTCAACGCAACCGTTTCGCCATGCCAATTG
25 GGGAAATCCCGGTAATGGCATGAATGCAAGACTTTACGTGAAAACGGGCTC
TGATTATACATGGCATAGCGGTCCTTTTACACGTATCAATAGCTCCAACTCA
GGAACAACGTTATCTTTTGATTAAACAACATCGAAAATATCATCATGTTAGG
GAAATAG

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SEQ ID NO:4**SEQUENCE CHARACTERISTICS:**

LENGTH: 468 amino acids

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TYPE: amino acid

TOPOLOGY: linear

005070 05958460

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 4

5 MKKKLSQIYHLIICTLIISVGIMGITTSPSAASTGFYVDGNTLYDANGQPFVMRGIN
HGHAWYKDTASTAIPAIAEQGANTIRIVLSDGGQWEKDDIDTIREVIELAEQNKM
VAVVEVHDATGRDSRSDLNRAVDYWIEMKDALIGKEDTVIINIANEWYGSWDGS
AWADGYIDVIPKLRLDAGLTHLTMVDAAGWGQYPQSIHDYGQDVFNADPLKNTM
FSIHMYEYAGGDANTVRSNIDRVIDQDLALVIGEFGRHTDGDVDEDTILSYSEE
10 TGTGWLAWSWKGNSTEWLDYLDLSEDWAGQHLTDWGNRIVHGADGLQETSKP
STVFTDDNGGHPEPPTATTLYDFEGSTQGWHGNSVTGGPWSVTEWGASGNY
SLKADVNLTSNSSHELYSEQSRNLHGYSQLNATVRHANWGNPGNGMNRALYV
KTGSDYTWHS GP FTRINSSNSGTTL SFDLNNIENIIMLGK

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SEQ ID NO:5

SEQUENCE CHARACTERISTICS:

LENGTH: 1029 base pairs

20 TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: genomic DNA

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SEQUENCE DESCRIPTION SEQ ID No:5

5' AAT TGG CGC ATA CTG TGT CGC CTG TGA ATC CTA ATG CCC AGC
AGA CAA CAA AAA CAG TGA TGA ACT GGC TTG CGC ACC TGC CGA ACC
30 GAA CGG AAA ACA GAG TCC TTT CCG GAG CGT TCG GAG GTT ACA GCC
ATG ACA CAT TTT CTA TGG CTG AGG CTG ATA GAA TCC GAA GCG CCA
CCG GGC AAT CGC CTG CTA TTT ATG GCT GCG ATT ATG CCA GAG GAT
GGC TTG AAA CAG CAA ATA TTG AAG ATT CAA TAG ATG TAA GCT GCA
ACG GCG ATT TAA TGT CGT ATT GGA AAA ATG GCG GAA TTC CGC AAA
35 TCA GTT TGC ACC TGG CGA ACC CTG CTT TTC AGT CAG GGC ATT TTA
AAA CAC CGA TTA CAA ATG ATC AGT ATA AAA ACA TAT TAG ATT CAG

CAA CAG CGG AAG GGA AGC GGC TAA ATG CCA TGC TCA GCA AAA TTG
CTG ACG GAC TTC AAG AGT TGG AGA ACC AAG GTG TGC CTG TTC TGT
TCA GGC CGC TGC ATG AAA TGA ACG GCG AAT GGT TTT GGT GGG GAC
TCA CAT CAT ATA ACC AAA AGG ATA ATG AAA GAA TCT CTC TAT ATA
5 AAC AGC TCT ACA AGA AAA TCT ATC ATT ATA TGA CCG ACA CAA GAG
GAC TTG ATC ATT TGA TTT GGG TTT ACT CTC CCG ACG CCA ACC GAG
ATT TTA AAA CTG ATT TTT ACC CGG GCG CGT CTT ACG TGG ATA TTG
TCG GAT TAG ATG CGT ATT TTC AAG ATG CCT ACT CGA TCA ATG GAT
ACG ATC AGC TAA CAG CGC TTA ATA AAC CAT TTG CTT TTA CAG AAG
10 TCG GCC CGC AAA CAG CAA ACG GCA GCT TCG ATT ACA GCC TGT TCA
TCA ATG CAA TAA AAC AAA AAT ATC CTA AAA CCA TTT ACT TTC TGG
CAT GGA ATG ATG AAT GGA GCG CAG CAG TAA ACA AGG GTG CTT CAG
CTT TAT ATC ATG ACA GCT GGA CAC TCA ACA AGG GAG AAA TAT GGA
ATG GTG ATT CTT TAA CGC CAA TCG TTG AGT GAA TCC GGG ATC 3'

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SEQ ID NO:6**SEQUENCE CHARACTERISTICS:**

20 LENGTH: 363 amino acids
TYPE: amino acid
TOPOLOGY: linear

MOLECULE TYPE: protein

25

SEQUENCE DESCRIPTION: SEQ ID NO: 6

ydhT 1
LFKKHTISLLIIFLLASAVLAKPIEAHTVSPVNPNAQQTTKTVMNWLHL 50
30 ydhT 51
PNRTENRVLSGAFGGYSHDTFSMAEADRIRSATGQSPAITYGCDYARGWLE 100
ydhT 101
TANIEDSIDVSCNGDLMSYWKNGGIPQISLHLANPAFQSGHFKTPITNDQ 150
ydhT 151
35 YKNILDSATAEGKRLNAMLSKIADGLQELENQGVPVLFRLHEMNGEWF 200

ydhT 201
WGLTSYNQKDNERISLYKQLYKKIYHYMTDTRGLDHLIWWYSPDANRDFK 250
ydhT 251
TDFYPGASYVDIVGLDAYFQDAYSINGYDQLTALNKPFAFTEVGPQTANG 300
5 ydhT 301
SFDYSLFINAIKQKYPKTIYFLAWNDEWSAAVNKGASALYHDSWTLNKGE 350
ydhT 351
IWNGDSLTPIVE*. 363

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